

WHAT IS CLAIMED IS:

1. A single exon nucleic acid microarray, comprising:

a plurality of nucleic acid probes addressably disposed upon a substrate,

wherein at least 50% of said nucleic acid probes include a fragment of no more than one exon of a eukaryotic genome, said fragment selectively hybridizable at high stringency to an expressed gene, wherein said plurality of nucleic acid probes averages at least 100 bp in length, and wherein said eukaryotic genome averages at least one intron per gene.

2. The microarray of claim 1, wherein at least 95% of said nucleic acid probes include a selectively hybridizable portion of no more than one exon of said eukaryotic genome.

3. The single exon nucleic acid microarray of claim 1, wherein at least 50% of said exon-including nucleic acid probes further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

4. The single exon nucleic acid microarray of claim 1, wherein at least 95% of said exon-including nucleic acid probes further comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the genome.

5. The single exon nucleic acid microarray of claim 1, wherein at least 50% of said exon-including nucleic acid probes comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and further comprise, contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

6. The single exon nucleic acid microarray of claim 1, wherein at least 95% of said exon-including nucleic acid probes comprise, contiguous to a first end of said fragment, a first intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome, and further comprise, contiguous to a second end of said fragment, a second intronic and/or intergenic sequence that is identically contiguous to said fragment in the human genome.

7. The single exon nucleic acid microarray of claim 1, wherein at least 50% of said exon-including nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

8. The single exon nucleic acid microarray of claim 1, wherein at least 95% of said exon-including nucleic acid probes lack prokaryotic and bacteriophage vector sequence.

9. The single exon nucleic acid microarray of claim 1, wherein at least 50% of said exon-including nucleic acid probes lack homopolymeric stretches of A or T.

10. The single exon nucleic acid microarray of claim 1, wherein at least 95% of said exon-including nucleic acid probes lack homopolymeric stretches of A or T.

11. The microarray of claim 1, wherein said eukaryotic genome averages at least two introns per gene.

12. The microarray of claim 1, wherein said eukaryotic genome averages at least three introns per gene.

13. The microarray of claim 1, wherein said eukaryotic genome averages at least five introns per gene.

14. The microarray of claim 1, wherein said genome is a human genome.

15. A method of identifying genes in a eukaryotic genome, comprising:

algorithmically predicting at least one of said gene's exons from genomic sequence of said eukaryote; and then

detecting hybridization of mRNA-derived nucleic acids to a nucleic acid probe having a selectively hybridizable portion identical in sequence to, or complementary in sequence to, said predicted exon,

wherein said probe is included within a single exon microarray according to any one of claims 1 - 14.

16. A method of measuring eukaryotic gene expression, comprising:

contacting the single exon microarray of any one of claims 1 - 14 with a first collection of detectably labeled nucleic acids, said first collection nucleic acids derived from mRNA of at least one eukaryotic tissue or cell type; and then

measuring the label detectably bound to each probe of said microarray.

17. The method of claim 16, further comprising comparing said measurement to a second measurement, said second measurement identically obtained using a second, control, collection of nucleic acids.

18. The method of claim 17, wherein said microarray is contacted simultaneously with said first and second collections of detectably labeled nucleic acids, wherein said first and second collection nucleic acids are distinguishably labeled.

19. A visual display of eukaryotic genomic sequence annotated with information about a predetermined biologic function, comprising:

a first visual element, each point along the length of which first visual element maps linearly and uniquely to a nucleotide of said genomic sequence;

a second visual element, first and second boundaries of which second visual element map linearly to a first and second nucleotide of said genomic sequence, wherein said first and second nucleotides delimit a region of said genomic sequence predicted to have said predetermined function; and

a third visual element, first and second boundaries of which third visual element map linearly to a first and second nucleotide of said genomic sequence, wherein said first and second nucleotides delimit a region of said genomic sequence experimentally confirmed to have said predetermined function.

20. The visual display of claim 19, wherein said display is electronic.